

Brannock, Michael

From: Brannock, Michael
Sent: Wednesday, August 02, 2006 12:01 PM
To: STIC-Biotech/ChemLib
Subject: 10622373

Please provide a full length search of SEQ ID NO: 1 and a full length and oligo search of SEQ ID NO: 2 against commercial, issued, and published sequence databases.

Thank you

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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:28:53 ; Search time 205 Seconds
(without alignments)
3172.457 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 1404
Sequence: 1 YWTFPVCTMTGAEIESGAQ.....AKELQGKTDNQNDPEGDQEN 1404

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2097797 seqs, 463214858 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2096646

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Published Applications AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	1404	100.0	1404	4	US-10-622-373-2
2	1404	100.0	1404	5	US-10-756-149-5141
3	60	4.3	60	4	US-10-639-067-156
4	57	4.1	225	4	US-10-108-260A-2706
5	57	4.1	655	4	US-10-108-260A-3501
6	57	4.1	838	4	US-10-622-373-6
7	54	3.8	54	4	US-10-639-067-157
8	50	3.6	50	5	US-10-776-013-606
9	50	3.6	50	5	US-10-776-013-607
10	44	3.1	44	4	US-10-639-067-155
11	34	2.4	34	4	US-10-764-425-138
12	20	1.4	20	5	US-10-776-013-601
13	20	1.4	20	5	US-10-776-013-602
14	20	1.4	20	5	US-10-776-013-603
15	20	1.4	20	5	US-10-776-013-604
16	20	1.4	20	5	US-10-776-013-605
17	16	1.1	74	3	US-09-864-761-35325
18	15	1.1	339	4	US-10-264-049-2738
19	13	0.9	177	4	US-10-104-047-3332
20	13	0.9	177	6	US-11-072-512-3332
21	10	0.7	23	5	US-10-862-195-708
22	9	0.6	265	4	US-10-398-037-15
23	8	0.6	84	4	US-10-424-599-223494
24	8	0.6	97	5	US-10-450-763-48794
25	8	0.6	99	3	US-09-925-297-842
26	8	0.6	113	4	US-10-767-701-47115
27	8	0.6	114	3	US-09-978-360A-726
28	8	0.6	114	3	US-09-978-360A-726
29	8	0.6	114	4	US-10-319-763-214
30	8	0.6	115	4	US-10-319-763-120
31	8	0.6	125	4	US-10-425-115-223773

32	8	0.6	185	4	US-10-425-114-48958	Sequence 48958, A
33	8	0.6	217	4	US-10-424-599-217689	Sequence 217689,
34	8	0.6	320	4	US-10-084-846A-84	Sequence 84, Appl
35	8	0.6	320	6	US-11-087-099-9834	Sequence 9834, Ap
36	8	0.6	397	4	US-10-767-701-45226	Sequence 45226, A
37	8	0.6	429	4	US-10-369-493-21679	Sequence 21679, A
38	8	0.6	433	4	US-10-369-493-20299	Sequence 20299, A
39	8	0.6	445	5	US-10-732-923-4200	Sequence 4200, Ap
40	8	0.6	447	4	US-10-424-599-250782	Sequence 250782,
41	8	0.6	454	4	US-10-369-493-8687	Sequence 8687, Ap
42	8	0.6	460	3	US-09-864-761-43042	Sequence 43042, A
43	8	0.6	469	4	US-10-369-493-22836	Sequence 22836, A
44	8	0.6	695	4	US-10-369-493-19882	Sequence 19882, A
45	8	0.6	888	4	US-10-282-122A-57155	Sequence 57155, A

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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:02:28 ; Search time 209 Seconds
(without alignments)
3071.444 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 7438
Sequence: 1 YWTFVVTCTMTGAEIESGAQ.....AKELGKTDNQNDPEGDQEN 1404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2589679 seqs, 457216429 residues

Total number of hits satisfying chosen parameters: 2589679

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_8:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*
10: geneseqp2006s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	7438	100.0	1404	8 ADJ57552	Adj57552 Human GAS
2	7380	99.2	1395	9 AEA23889	Aea23889 Human PRO
3	2084.5	28.0	838	4 AAM79102	Aam79102 Human pro
4	2084.5	28.0	838	8 ADJ57556	Adj57556 Human GAS
5	2077.5	27.9	838	8 ADQ66022	Adq66022 Novel hum
6	1794.5	24.1	901	4 AAM80086	Aam80086 Human pro
7	1794.5	24.1	901	7 ADC32958	Adc32958 Human nov
8	1677.5	22.6	635	5 ABB08788	Abb08788 Human LAM
9	1527.5	20.5	655	7 ADM04816	Adm04816 Human pro
10	1527.5	20.5	655	9 AEC87746	Aec87746 Human cDN
11	943	12.7	225	7 ADM04021	Adm04021 Human pro
12	943	12.7	225	9 AEC86951	Aec86951 Human cDN
13	896	12.0	2338	8 ABO58348	Abo58348 Human gen
14	732.5	9.8	2367	4 AAU31850	Aau31850 Novel hum
15	722.5	9.7	339	5 ABP41606	Abp41606 Human ova
16	720.5	9.7	574	4 ABG07996	Abg07996 Novel hum
17	682.5	9.2	570	7 ADJ69585	Adj69585 Human hea
18	674.5	9.1	547	6 ABR44353	Abr44353 Human lar
19	674.5	9.1	547	7 ADC31273	Adc31273 Human nov
20	674.5	9.1	547	7 ADC33434	Adc33434 Human p60
21	652.5	8.8	539	7 ADC33432	Adc33432 Rat p60TR
22	630.5	8.5	177	7 ADB65178	Adb65178 Human pro
23	625.5	8.4	176	9 ADV77071	Adv77071 Huntingto
24	550.5	7.4	558	3 AAB42722	Aab42722 Human ORF
25	550.5	7.4	558	4 AAB95263	Aab95263 Human pro
26	550.5	7.4	558	5 ABP69780	Abp69780 Human pol
27	550.5	7.4	558	5 ABB75717	Abb75717 Human cel

28	529	7.1	122	5	ABP07806	Abp07806	Human	ORF
29	473	6.4	310	9	AEA20290	Aea20290	Novel	hum
30	454	6.1	387	7	ADI60400	Adi60400	Secreted	
31	454	6.1	387	9	AEA21102	Aea21102	Novel	hum
32	444.5	6.0	367	7	ADI60171	Adi60171	Secreted	
33	360	4.8	453	4	AAM93332	Aam93332	Human	pol
34	360	4.8	453	4	AAG67208	Aag67208	Amino	aci
35	360	4.8	453	4	AAU28175	Aau28175	Novel	hum
36	360	4.8	453	4	AAG67135	Aag67135	Amino	aci
37	360	4.8	453	8	ADL30830	Adl30830	Human	pro
38	349.5	4.7	379	2	AAY17220	Aay17220	Human	sec
39	349.5	4.7	379	4	AAU38990	Aau38990	Human	sec
40	349.5	4.7	379	5	ABB55699	Abb55699	Human	pol
41	349.5	4.7	379	9	ADW09091	Adw09091	Human	sec
42	345	4.6	264	3	AAB32088	Aab32088	Human	sec
43	345	4.6	337	4	AAG67776	Aag67776	Amino	aci
44	345	4.6	342	4	AAB27240	Aab27240	Human	EXM
45	345	4.6	342	7	ADJ69028	Adj69028	Human	hea

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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:12:27 ; Search time 56 Seconds
(without alignments)
2194.518 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 7438
Sequence: 1 YWTFVVTCTMTGAEIESGAQ.....AKELQGKTDNQNDPEGDQEN 1404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 650591 seqs, 87530628 residues

Total number of hits satisfying chosen parameters: 650591

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_AA:*
1: /EMC_Celerra_SIDS3/ptodata/2/iaa/5_COMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/iaa/6_COMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/iaa/7_COMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/iaa/H_COMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/iaa/RE_COMB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	630.5	8.5	177	2	US-10-104-047-3332 Sequence 3332, Ap
2	345	4.6	337	2	US-09-780-996A-9 Sequence 9, Appli
3	345	4.6	337	2	US-10-726-721A-9 Sequence 9, Appli
4	345	4.6	379	2	US-09-193-266-1 Sequence 1, Appli
5	284	3.8	1070	2	US-09-902-540-13861 Sequence 13861, A
6	245	3.3	1805	1	US-07-853-913-2 Sequence 2, Appli
7	221.5	3.0	1858	2	US-09-902-540-12643 Sequence 12643, A
8	221	3.0	1091	2	US-09-949-016-8595 Sequence 8595, Ap
9	217	2.9	1088	2	US-09-130-242-2 Sequence 2, Appli
10	217	2.9	1088	2	US-09-583-610D-2 Sequence 2, Appli
11	217	2.9	1088	2	US-09-949-016-6935 Sequence 6935, Ap
12	213.5	2.9	2476	2	US-09-824-574-7 Sequence 7, Appli
13	210.5	2.8	1781	2	US-09-961-403-13 Sequence 13, Appl
14	206	2.8	1780	1	US-08-769-309A-5 Sequence 5, Appli
15	206	2.8	1780	2	US-08-994-570-5 Sequence 5, Appli
16	202	2.7	1618	1	US-07-853-913-4 Sequence 4, Appli
17	202	2.7	1618	2	US-09-538-092-1143 Sequence 1143, Ap
18	202	2.7	1618	2	US-09-731-255-2 Sequence 2, Appli
19	202	2.7	1618	2	US-10-136-891-2 Sequence 2, Appli
20	196	2.6	2375	2	US-09-538-092-1131 Sequence 1131, Ap
21	194	2.6	674	2	US-08-893-852A-1 Sequence 1, Appli
22	193.5	2.6	1596	2	US-08-978-277A-4 Sequence 4, Appli
23	192.5	2.6	203	2	US-10-094-749-1808 Sequence 1808, Ap
24	190.5	2.6	1020	2	US-09-538-092-911 Sequence 911, App
25	188	2.5	3924	2	US-09-538-092-1246 Sequence 1246, Ap
26	184.5	2.5	1018	1	US-08-072-610-2 Sequence 2, Appli
27	184.5	2.5	1018	1	US-08-719-822B-2 Sequence 2, Appli
28	184.5	2.5	1018	2	US-09-092-458-2 Sequence 2, Appli
29	184.5	2.5	1018	2	US-08-719-821C-2 Sequence 2, Appli
30	181.5	2.4	1444	2	US-09-949-016-9652 Sequence 9652, Ap

31	181.5	2.4	2004	2	US-09-538-092-1371	Sequence 1371, Ap
32	181.5	2.4	2004	2	US-09-949-016-6756	Sequence 6756, Ap
33	181	2.4	901	2	US-09-248-796A-14747	Sequence 14747, A
34	181	2.4	1346	1	US-08-635-121-2	Sequence 2, Appli
35	181	2.4	1346	2	US-08-978-277A-2	Sequence 2, Appli
36	180.5	2.4	793	2	US-09-538-092-1271	Sequence 1271, Ap
37	176	2.4	1786	2	US-08-973-462-8	Sequence 8, Appli
38	172.5	2.3	1878	2	US-09-949-016-8902	Sequence 8902, Ap
39	172.5	2.3	1878	2	US-09-949-016-8903	Sequence 8903, Ap
40	171.5	2.3	3224	1	US-08-705-660-34	Sequence 34, Appl
41	171.5	2.3	3224	2	US-08-989-045-34	Sequence 34, Appl
42	171.5	2.3	3224	2	US-09-538-092-1161	Sequence 1161, Ap
43	171.5	2.3	3224	2	US-09-315-355A-34	Sequence 34, Appl
44	168	2.3	706	2	US-10-104-047-3843	Sequence 3843, Ap
45	168	2.3	2079	2	US-09-949-016-8301	Sequence 8301, Ap

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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:13:22 ; Search time 205 Seconds
(without alignments)
3172.457 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 7438
Sequence: 1 YWTFVVTCTMTGAEIESGAQ.....AKELQGKTDNQNDPEGDQEN 1404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2097797 seqs, 463214858 residues

Total number of hits satisfying chosen parameters: 2097797

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	7438	100.0	1404	4	US-10-622-373-2
2	7438	100.0	1404	5	US-10-756-149-5141
3	2084.5	28.0	838	4	US-10-622-373-6
4	1527.5	20.5	655	4	US-10-108-260A-3501
5	943	12.7	225	4	US-10-108-260A-2706
6	896	12.0	2338	4	US-10-029-386-31982
7	722.5	9.7	339	4	US-10-264-049-2738
8	720.5	9.7	574	5	US-10-450-763-38355
9	682.5	9.2	570	4	US-10-408-765A-1391
10	674.5	9.1	547	5	US-10-466-634-8
11	652.5	8.8	539	5	US-10-466-634-6
12	630.5	8.5	177	4	US-10-104-047-3332
13	630.5	8.5	177	6	US-11-072-512-3332
14	360	4.8	453	4	US-10-220-381-10
15	360	4.8	453	4	US-10-291-172-344
16	360	4.8	453	4	US-10-221-278-344
17	360	4.8	453	4	US-10-204-751A-3
18	349.5	4.7	379	3	US-09-729-674-4
19	349.5	4.7	379	5	US-10-913-553-4
20	345	4.6	337	3	US-09-780-996-9
21	345	4.6	337	4	US-10-726-721-9
22	345	4.6	342	4	US-10-408-765A-834
23	345	4.6	379	4	US-10-028-072-216
24	345	4.6	379	4	US-10-140-808-216
25	345	4.6	379	4	US-10-121-049-216
26	345	4.6	379	4	US-10-123-904-216
27	345	4.6	379	4	US-10-140-470-216
28	345	4.6	379	4	US-10-175-746-216
29	345	4.6	379	4	US-10-176-918-216
30	345	4.6	379	4	US-10-176-921-216
31	345	4.6	379	4	US-10-137-865-216

32	345	4.6	379	4	US-10-140-474-216	Sequence 216, App
33	345	4.6	379	4	US-10-142-431-216	Sequence 216, App
34	345	4.6	379	4	US-10-143-114-216	Sequence 216, App
35	345	4.6	379	4	US-10-142-419-216	Sequence 216, App
36	345	4.6	379	4	US-10-123-262-216	Sequence 216, App
37	345	4.6	379	4	US-10-142-423-216	Sequence 216, App
38	345	4.6	379	4	US-10-121-050-216	Sequence 216, App
39	345	4.6	379	4	US-10-141-755-216	Sequence 216, App
40	345	4.6	379	4	US-10-143-032-216	Sequence 216, App
41	345	4.6	379	4	US-10-123-108-216	Sequence 216, App
42	345	4.6	379	4	US-10-123-236-216	Sequence 216, App
43	345	4.6	379	4	US-10-123-261-216	Sequence 216, App
44	345	4.6	379	4	US-10-140-921-216	Sequence 216, App
45	345	4.6	379	4	US-10-140-928-216	Sequence 216, App

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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:14:23 ; Search time 40 Seconds
(without alignments)
2348.683 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 7438
Sequence: 1 YWTFVVTCTMTGAEIESGAQ.....AKELQGKTDNQNDPEGDQEN 1404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 236815 seqs, 66914042 residues

Total number of hits satisfying chosen parameters: 236815

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA_New:*
1: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
2: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
3: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
4: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
5: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
6: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
7: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
8: /EMC_Celerra_SIDS3/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	1527.5	20.5	655	7	US-11-293-697-3501	Sequence 3501, Ap
2	943	12.7	225	7	US-11-293-697-2706	Sequence 2706, Ap
3	328.5	4.4	632	6	US-10-505-928-377	Sequence 377, App
4	302	4.1	323	7	US-11-354-653-87	Sequence 87, Appl
5	302	4.1	343	7	US-11-354-653-33	Sequence 33, Appl
6	292	3.9	308	7	US-11-354-653-136	Sequence 136, App
7	281.5	3.8	319	7	US-11-354-653-124	Sequence 124, App
8	281.5	3.8	354	7	US-11-354-653-127	Sequence 127, App
9	257	3.5	238	7	US-11-354-653-115	Sequence 115, App
10	211	2.8	1303	6	US-10-449-902-55274	Sequence 55274, A
11	195	2.6	674	7	US-11-040-219-2	Sequence 2, Appli
12	183	2.5	939	6	US-10-449-902-41543	Sequence 41543, A
13	175	2.4	1972	7	US-11-253-190-1	Sequence 1, Appli
14	171	2.3	1826	7	US-11-221-332-44	Sequence 44, Appl
15	166	2.2	509	6	US-10-449-902-38181	Sequence 38181, A
16	163	2.2	1614	6	US-10-505-928-199	Sequence 199, App
17	162.5	2.2	935	6	US-10-449-902-42274	Sequence 42274, A
18	161.5	2.2	284	7	US-11-354-653-121	Sequence 121, App
19	161	2.2	991	7	US-11-165-586-62	Sequence 62, Appl
20	160	2.2	738	6	US-10-953-349-5388	Sequence 5388, Ap
21	160	2.2	763	6	US-10-953-349-5387	Sequence 5387, Ap
22	158.5	2.1	3256	6	US-10-505-928-357	Sequence 357, App
23	157.5	2.1	1491	7	US-11-056-355B-101109	Sequence 101109,
24	157.5	2.1	1491	7	US-11-056-355B-112348	Sequence 112348,
25	157.5	2.1	1495	7	US-11-056-355B-101108	Sequence 101108,
26	157.5	2.1	1495	7	US-11-056-355B-112347	Sequence 112347,
27	156	2.1	1863	6	US-10-480-434A-16	Sequence 16, Appl
28	155	2.1	1251	6	US-10-953-349-8779	Sequence 8779, Ap
29	154.5	2.1	3934	7	US-11-165-586-20	Sequence 20, Appl

30	153	2.1	1263	6	US-10-540-898-539	Sequence 539, App
31	153	2.1	1466	7	US-11-056-355B-101110	Sequence 101110,
32	153	2.1	1466	7	US-11-056-355B-112349	Sequence 112349,
33	153	2.1	1498	7	US-11-266-446-94	Sequence 94, Appl
34	153	2.1	1828	7	US-11-056-355B-91730	Sequence 91730, A
35	153	2.1	1828	7	US-11-056-355B-95486	Sequence 95486, A
36	153	2.1	1999	7	US-11-056-355B-91729	Sequence 91729, A
37	153	2.1	1999	7	US-11-056-355B-95485	Sequence 95485, A
38	153	2.1	2008	7	US-11-056-355B-91728	Sequence 91728, A
39	153	2.1	2008	7	US-11-056-355B-95484	Sequence 95484, A
40	152	2.0	850	6	US-10-449-902-41508	Sequence 41508, A
41	151.5	2.0	584	7	US-11-293-697-4839	Sequence 4839, Ap
42	151	2.0	260	7	US-11-354-653-133	Sequence 133, App
43	151	2.0	295	7	US-11-354-653-130	Sequence 130, App
44	149.5	2.0	1032	6	US-10-449-902-45139	Sequence 45139, A
45	149	2.0	710	6	US-10-449-902-41319	Sequence 41319, A

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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:06:57 ; Search time 53 Seconds
(without alignments)
2548.837 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 7438
Sequence: 1 YWTFPVTCTMTGAEIESGAQ.....AKELQGKTDNQNDPEGDQEN 1404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	7380	99.2	1395	2	T00068	hypothetical prote
2	360	4.8	453	2	JC7582	armadillo(arm) rep
3	342.5	4.6	1094	2	A53435	vesicular transpor
4	328.5	4.4	632	2	T00084	hypothetical prote
5	300	4.0	2550	2	B53435	vesicular transpor
6	284.5	3.8	5327	2	T13564	microtubule-associ
7	283.5	3.8	1110	2	I51116	NF-180 - sea lampr
8	252.5	3.4	1829	2	T24583	hypothetical prote
9	245	3.3	1805	2	A34736	nestin - rat
10	238.5	3.2	1804	2	T34518	nestin - golden ha
11	229	3.1	913	2	T52485	neurofilament prot
12	228	3.1	1871	2	D96796	probable heat shoc
13	220.5	3.0	1233	2	S56271	hypothetical prote
14	217.5	2.9	1052	1	A44937	kinetoplast-associ
15	210.5	2.8	3488	2	T34418	hypothetical prote
16	210	2.8	1132	2	T43483	translation initia
17	206	2.8	4574	2	G02520	plectin - human
18	202	2.7	1618	2	S21424	nestin - human
19	198.5	2.7	1403	2	T11583	probable translati
20	198	2.7	2261	2	T20978	hypothetical prote
21	197.5	2.7	837	2	JN0292	antigen 332 - mala
22	197.5	2.7	1567	2	T03730	antigen containing
23	197.5	2.7	2241	2	T20971	hypothetical prote
24	196.5	2.6	4687	1	A39638	plectin - rat
25	196	2.6	1526	2	A45605	mature-parasite-in
26	195	2.6	4684	2	A59404	plectin [imported]
27	193.5	2.6	1684	2	JW0057	gravin - human
28	193.5	2.6	4385	2	T29042	hypothetical prote
29	193	2.6	2364	2	A56577	microtubule-associ
30	192	2.6	5170	2	T15348	hypothetical prote
31	190.5	2.6	1020	1	QFHUH	neurofilament trip
32	190	2.6	1621	2	A82255	hypothetical prote
33	189.5	2.5	2774	2	A43359	microtubule-associ

34	188	2.5	3924	2	S37431	ankyrin 2, neurona
35	186	2.5	6642	2	T29757	protein UNC-89 - C
36	185.5	2.5	2464	1	QRMSF1	microtubule-associ
37	184.5	2.5	1641	2	I38614	helicase II - huma
38	183.5	2.5	2484	2	T26216	hypothetical prote
39	183.5	2.5	2607	2	T26215	hypothetical prote
40	183	2.5	407	1	EDBEQ3	immediate-early pr
41	181	2.4	1346	2	A57376	probable regulator
42	180.5	2.4	721	2	S29795	hypothetical prote
43	180.5	2.4	793	1	JH0628	caldesmon - human
44	180	2.4	839	2	E84824	hypothetical prote
45	180	2.4	1589	2	C44766	defective chorion-

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OM protein - protein search, using sw model

Run on: August 7, 2006, 13:03:02 ; Search time 335 Seconds
(without alignments)
3876.782 Million cell updates/sec

Title: US-10-622-373-2
Perfect score: 7438
Sequence: 1 YWTFVTCMTGAEIESGAQ.....AKELGKTDNQNDPEGDQEN 1404

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2849598 seqs, 925015592 residues

Total number of hits satisfying chosen parameters: 2849598

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_7.2:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	7437	99.9	1404	2	O43168_HUMAN
2	7373	99.1	1395	2	Q5JY77_HUMAN
3	4045	54.4	1350	2	Q8CHF4_MOUSE
4	4029	54.2	1347	2	Q5U4C1_MOUSE
5	3976.5	53.5	1346	2	Q920R4_RAT
6	2721.5	36.6	874	2	Q8R095_MOUSE
7	2567.5	34.5	957	2	Q6PD32_MOUSE
8	2093.5	28.1	838	2	Q5R7U0_PONPY
9	2084.5	28.0	838	2	Q96D09_HUMAN
10	1527.5	20.5	655	2	Q8N8W9_HUMAN
11	1495.5	20.1	405	2	Q8BYK9_MOUSE
12	1044	14.0	379	2	Q8BKR8_MOUSE
13	961	12.9	347	2	Q8BUN4_MOUSE
14	757.5	10.2	995	2	Q8K2R3_MOUSE
15	682.5	9.2	570	2	Q9C0G2_HUMAN
16	674.5	9.1	547	2	Q6PI77_HUMAN
17	674.5	9.1	547	2	Q9BE11_MACFA
18	652.5	8.8	539	2	Q71HP2_RAT
19	631.5	8.5	352	2	Q8BUY8_MOUSE
20	630.5	8.5	177	2	Q8NAB4_HUMAN
21	629.5	8.5	539	2	Q6PB60_MOUSE
22	550.5	7.4	558	1	ARMX5_HUMAN
23	539	7.2	606	1	ARMX5_MOUSE
24	536.5	7.2	558	1	ARMX5_PONPY
25	521	7.0	497	2	Q8R0B3_MOUSE
26	475	6.4	342	2	Q5H9K7_HUMAN
27	431	5.8	340	2	Q8R103_MOUSE
28	378.5	5.1	2197	2	Q57TX7_TRYPY
29	360	4.8	453	1	ARMX1_HUMAN
30	355	4.8	360	2	Q69ZD0_MOUSE
31	350.5	4.7	461	1	ARMX1_RAT
32	350	4.7	453	1	ARMX1_PONPY
33	346	4.7	456	1	ARMX1_MOUSE
34	345	4.6	379	1	ARMX3_HUMAN
35	345	4.6	379	1	ARMX3_PONPY

36	342.5	4.6	1094	2	Q26774_9TRYP	Q26774 trypanosoma
37	341	4.6	379	1	ARMX3_MOUSE	Q8bhs6 mus musculu
38	341	4.6	379	1	ARMX3_RAT	Q5xid7 rattus norv
39	328.5	4.4	632	1	ARMX2_HUMAN	Q71311 homo sapien
40	324.5	4.4	624	2	Q5RfK2_PONPY	Q5rfk2 pongo pygma
41	320	4.3	2316	1	UAFA_STAS1	Q4a0v8 staphylococ
42	310	4.2	306	2	Q9CZ87_MOUSE	Q9cz87 mus musculu
43	310	4.2	306	2	Q9D0L7_MOUSE	Q9d0l7 mus musculu
44	310	4.2	1209	2	Q3XRG5_9PROT	Q3xrg5 magnetococc
45	307	4.1	308	2	Q9BTM6_HUMAN	Q9btm6 homo sapien